We Claim:

5   1.   A crystal of a 30S subunit having a tetragonal space group $P4_12_12$ with unit cell dimensions of a = 401.375 Å, b = 401.375 Å, c = 175.887 Å.

2.   A crystal of a 30S subunit having a tetragonal space group $P4_12_12$ with unit cell dimensions of a = 401.4 Å, b = 401.4 Å, c = 175.9 Å.

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3.   A crystal of a 30S ribosomal subunit having a resolution better (numerically less) than about 3 Å.

4.   A crystal a 30S ribosomal subunit having the structure defined by the co-ordinates of Table 15   1.

5.   A computer-based method of rational drug design which comprises:
    providing the structure of a 30S ribosomal subunit as defined by the coordinates of Table 1;
    providing the structure of a candidate modulator molecule; and
20   fitting the structure of the candidate to the structure of the 30S of Table 1.

6.   A computer-based method for identifying a potential inhibitor of the 30S ribosome comprising the steps of:
    a. employing a three-dimensional structure of 30S, or at least one sub-domain thereof, to
25   characterise at least one active site, the three-dimensional structure being defined by atomic coordinate data according to Table 1; and
    b. identifying the potential inhibitor by designing or selecting a compound for interaction with the active site.

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7.   The method of claim 6 which further comprises:
    c. obtaining or synthesising the potential inhibitor;
    d. contacting the potential inhibitor with 30S to determine the ability of said inhibitor to interact with the 30S.

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8.   The method of claim 6 which further comprises:

        c. obtaining or synthesising said potential ligand;

        d. forming a complex of 30S and said potential ligand; and

5.   e. analysing said complex by X-ray crystallography to determine the ability of said potential ligand

        to interact with 30S.

9.   A method for the determination of the structure of a bacterial 30S from a species other than

T. thermophilus which method comprises:

10   (a)   crystallising the 30S of said species to obtain a crystal;

                (b)   performing X-ray crystallography on said crystal to obtain X-ray diffraction data;

                (c)   providing the structure data of Table 1; and

                (d)   using molecular replacement to calculate an electron density map of the 30S.

15   10.   A computer system, intended to generate structures and/or perform rational drug design for

the 30S ribosome or complexes of the 30S ribosome with a potential modulator, the system

containing either (a) atomic coordinate data according to Table 1, said data defining the three-

dimensional structure of 30S or at least one sub-domain thereof, or (b) structure factor data for 30S,

said structure factor data being derivable from the atomic coordinate data of Table 1.

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11.   A computer readable media with either (a) atomic coordinate data according to Table 1

recorded thereon, said data defining the three-dimensional structure of the 30S ribosome, at least one

atom or at least one sub-domain thereof, or (b) structure factor data for the 30S ribosome recorded

thereon, the structure factor data being derivable from the atomic coordinate data of Table 1.

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